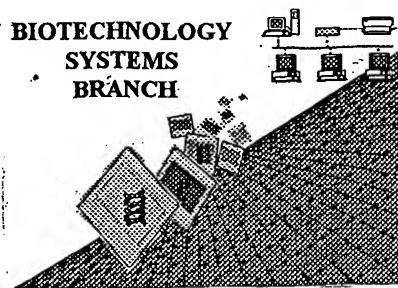BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/024,036_

Source: _OIPE_

Date Processed by STIC: _1/15/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**, **EFS Submission User Manual - ePAVE**)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
      Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/024,036_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

```
 4 <110> APPLICANT: Bandaru, Rajasekhar
 6 <120> TITLE OF INVENTION: 68730 and 69112, Protein Kinase
 7         Molecules and Uses Therefor
10 <130> FILE REFERENCE: MPI2000-521P1R(M)
12 <140> CURRENT APPLICATION NUMBER: US/10/024,036
12 <141> CURRENT FILING DATE: 2001-12-17
12 <150> PRIOR APPLICATION NUMBER: 60/258222
13 <151> PRIOR FILING DATE: 2000-12-22
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1772
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <220> FEATURE:
25 <221> NAME/KEY: 5'UTR
26 <222> LOCATION: (1)...(168)
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (9)...(1242)
31 <221> NAME/KEY: 3'UTR
32 <222> LOCATION: (1243)...(1772)
34 <400> SEQUENCE: 1
```

see p. 5, too

Does Not Comply
Corrected Diskette Needed

→ *see item 9 on Eva Summary Sheet*

```
W-->35 ncngnncg cgg cgg cgt gcg cac gag cga aag agg aaa ctg cag agg agg  50
    36          Arg Arg Arg Ala His Glu Arg Lys Arg Lys Leu Gln Arg Arg
    37          1               5                   10
    39 aag ctg cgc cgc agc ccg agc cgc ccg gca tcc ccg ccg cct ctg cgc  98
    40 Lys Leu Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg
    41 15              20                  25                  30
    43 ccg cgc cgc gcc ccc ggc gcc ccc tcc cca gcg cgc ccc cgg ccg ctc 146
    44 Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
    45              35                  40                  45
    47 ctc cgc gcc gcg ctc gtc ggc cat ggc ccg gga gaa cgg cga gag cag 194
    48 Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
    49              50                  55                  60
    51 ctc ctc ctg gaa aaa gca agc tga aga cat caa gaa gat ctt cga gtt 242
    52 Leu Leu Leu Glu Lys Ala Ser  *  Arg His Gln Glu Asp Leu Arg Val
    53          65                  70                  75
    55 caa aga gac cct cgg aac cgg ggc ctt ttc cga agt ggt ttt agc tga 290
    56 Gln Arg Asp Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser  *
    57          80                  85                  90
    59 aga gaa ggc aac tgg caa gct ctt tgc tgt gaa gtg tat ccc taa gaa 338
    60 Arg Glu Gly Asn Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro  *  Glu
    61          95                  100                 105
    63 ggc gct gaa ggg caa gga aag cag cat aga gaa tga gat agc cgt cct 386
    64 Gly Ala Glu Gly Gln Gly Lys Gln His Arg Glu  *  Asp Ser Arg Pro
    65          110                 115                 120
    67 gag aaa gat taa gca tga aaa tat tgt tgc cct gga aga cat tta tga 434
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

```
 68 Glu Lys Asp  *  Ala  *  Lys Tyr Cys Cys Pro Gly Arg His Leu  *
 69         125                         130             135
 71 aag ccc aaa tca cct gta ctt ggt cat gca gct ggt gtc cgg tgg aga    482
 72 Lys Pro Lys Ser Pro Val Leu Gly His Ala Ala Gly Val Arg Trp Arg
 73             140                 145                 150
 75 gct gtt tga ccg gat agt gga gaa ggg gtt tta tac aga gaa gga tgc    530
 76 Ala Val  *  Pro Asp Ser Gly Glu Gly Val Leu Tyr Arg Glu Gly Cys
 77             155                 160                 165
 79 cag cac tct gat ccg cca agt ctt gga cgc cgt gta cta tct cca cag    578
 80 Gln His Ser Asp Pro Pro Ser Leu Gly Arg Arg Val Leu Ser Pro Gln
 81             170                 175                 180
 83 aat ggg cat cgt cca cag aga cct caa gcc cga aaa tct ctt gta cta    626
 84 Asn Gly His Arg Pro Gln Arg Pro Gln Ala Arg Lys Ser Leu Val Leu
 85         185                 190                 195
 87 cag tca aga tga gga gtc caa aat aat gat cag tga ctt tgg att gtc    674
 88 Gln Ser Arg  *  Gly Val Gln Asn Asn Asp Gln  *  Leu Trp Ile Val
 89         200                 205                 210
 91 aaa aat gga ggg caa agg aga tgt gat gtc cac tgc ctg tgg aac tcc    722
 92 Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys Leu Trp Asn Ser
 93         215                 220                 225
 95 agg cta tgt cgc tcc tga agt cct cgc cca gaa acc tta cag caa agc    770
 96 Arg Leu Cys Arg Ser  *  Ser Pro Arg Pro Glu Thr Leu Gln Gln Ser
 97         230                 235                 240
 99 cgt tga ctg ctg gtc cat cgg agt gat tgc cta cat ctt gct ctg cgg    818
100 Arg  *  Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala Leu Arg
101         245                 250                 255
103 cta ccc tcc ttt tta tga tga aaa tga ctc caa gct ctt tga gca gat    866
104 Leu Pro Ser Phe Leu  *   *  Lys  *  Leu Gln Ala Leu  *  Ala Asp
105         260                         265                 270
107 cct caa ggc gga ata tga gtt tga ctc tcc cta ctg gga tga cat ctc    914
108 Pro Gln Gly Gly Ile  *  Val  *  Leu Ser Leu Leu Gly  *  His Leu
109                 275                         280
111 cga ctc tgc aaa aga ctt cat tcg gaa cct gat gga gaa gga ccc gaa    962
112 Arg Leu Cys Lys Arg Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu
113         285                 290                 295
115 taa aag ata cac gtg tga gca ggc agc tcg gca ccc atg gat cgc tgg   1010
116  *  Lys Ile His Val  *  Ala Gly Ser Ser Ala Pro Met Asp Arg Trp
117         300                 305                 310
119 tga cac agc cct caa caa aaa cat cca cga gtc cgt cag cgc cca gat   1058
120  *  His Ser Pro Gln Gln Lys His Pro Arg Val Arg Gln Arg Pro Asp
121         315                 320                 325
123 ccg gaa aaa ctt tgc caa gag caa atg gag aca agc att taa tgc cac   1106
124 Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile  *  Cys His
125         330                 335                 340
127 ggc cgt cgt gag aca tat gag aaa act aca cct cgg cag cag cct gga   1154
128 Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly
129         345                 350                 355
131 cag ttc aaa tgc aag tgt ttc gag cag cct cag ttt ggc cag cca aaa   1202
132 Gln Phe Lys Cys Lys Cys Phe Glu Gln Pro Gln Phe Gly Gln Pro Lys
```

1/15/02

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

```
133 360                  365              370              375
135 aga ctg tgc gta tgt agc aaa acc aga atc cct cag ctg a cactgaagac 1252
136 Arg Leu Cys Val Cys Ser Lys Thr Arg Ile Pro Gln Leu
137               380               385
139 gagcctgggg tggagaggag ggagccggca tctgccgagc acctcctgtt tgccaggcgc 1312
140 tttctatact taatcccatg tcatgcgacc ctaggacttt ttttaacatg taatcactgg 1372
141 gccgggtgca gtggctcacg cctgtaatcc caacactttg ggaggctgag gcaggaggac 1432
142 tgtttgagtt caggagtttt aagaccagcc tgaccaacat ggtgaaaccc catctctact 1492
143 aaaatataaa aattagccgg gtgtggtggc gagcacctgt aatgtcagct acttgggagg 1552
144 ctgaggcagg agaatcactt gaacccagga agcggaggtt gcaatgagct gagatcacac 1612
145 cactgcactc cagcctgggt gacagattga gactccctct caaaaaaaaa agggaaatca 1672
146 ttgaacactc gtggaaccct aggtattgca tattccattt acggtttggg aatccagggc 1732
147 tcaagtcctc gcaggggtac cgagctcgag atcgtaatca                        1772
149 <210> SEQ ID NO: 2
150 <211> LENGTH: 388
151 <212> TYPE: PRT
152 <213> ORGANISM: Human
154 <400> SEQUENCE: 2
155 Arg Arg Arg Ala His Glu Arg Lys Arg Lys Leu Gln Arg Arg Lys Leu
156 1               5                   10                  15
157 Arg Arg Ser Pro Ser Arg Pro Ala Ser Pro Pro Pro Leu Arg Pro Arg
158           20                  25                  30
159 Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu Leu Arg
160           35                  40                  45
161 Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln Leu Leu
162      50                  55                  60
163 Leu Glu Lys Ala Ser Arg His Gln Glu Asp Leu Arg Val Gln Arg Asp
164 65                  70                  75                  80
165 Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser Arg Glu Gly Asn
166               85                  90                  95
167 Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro Glu Gly Ala Glu Gly Gln
168           100                 105                 110
169 Gly Lys Gln His Arg Glu Asp Ser Arg Pro Glu Lys Asp Ala Lys Tyr
170           115                 120                 125
171 Cys Cys Pro Gly Arg His Leu Lys Pro Lys Ser Pro Val Leu Gly His
172      130                 135                 140
173 Ala Ala Gly Val Arg Trp Arg Ala Val Pro Asp Ser Gly Glu Gly Val
174 145                 150                 155                 160
175 Leu Tyr Arg Glu Gly Cys Gln His Ser Asp Pro Pro Ser Leu Gly Arg
176               165                 170                 175
177 Arg Val Leu Ser Pro Gln Asn Gly His Arg Pro Gln Arg Pro Gln Ala
178           180                 185                 190
179 Arg Lys Ser Leu Val Leu Gln Ser Arg Gly Val Gln Asn Asn Asp Gln
180           195                 200                 205
181 Leu Trp Ile Val Lys Asn Gly Gly Gln Arg Arg Cys Asp Val His Cys
182      210                 215                 220
183 Leu Trp Asn Ser Arg Leu Cys Arg Ser Ser Pro Arg Pro Glu Thr Leu
184 225                 230                 235                 240
185 Gln Gln Ser Arg Leu Leu Val His Arg Ser Asp Cys Leu His Leu Ala
```

```
186                        245                      250                      255
187 Leu Arg Leu Pro Ser Phe Leu Lys Leu Gln Ala Leu Ala Asp Pro Gln
188                        260                      265                      270
189 Gly Gly Ile Val Leu Ser Leu Leu Gly His Leu Arg Leu Cys Lys Arg
190                        275                      280                      285
191 Leu His Ser Glu Pro Asp Gly Glu Gly Pro Glu Lys Ile His Val Ala
192           290                      295                      300
193 Gly Ser Ser Ala Pro Met Asp Arg Trp His Ser Pro Gln Gln Lys His
194 305                      310                      315                      320
195 Pro Arg Val Arg Gln Arg Pro Asp Pro Glu Lys Leu Cys Gln Glu Gln
196                        325                      330                      335
197 Met Glu Thr Ser Ile Cys His Gly Arg Arg Glu Thr Tyr Glu Lys Thr
198           340                      345                      350
199 Thr Pro Arg Gln Gln Pro Gly Gln Phe Lys Cys Lys Cys Phe Glu Gln
200           355                      360                      365
201 Pro Gln Phe Gly Gln Pro Lys Arg Leu Cys Val Cys Ser Lys Thr Arg
202           370                      375                      380
203 Ile Pro Gln Leu
204 385
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1074
209 <212> TYPE: DNA
210 <213> ORGANISM: Human
212 <400> SEQUENCE: 3
213 atggcccggg agaacggcga gagcagctcc tcctggaaaa agcaagctga agacatcaag   60
214 aagatcttcg agttcaaaga gaccctcgga accggggcct tttccgaagt ggttttagct  120
215 gaagagaagg caactggcaa gctctttgct gtgaagtgta tccctaagaa ggcgctgaag  180
216 ggcaaggaaa gcagcataga gaatgagata gccgtcctga gaaagattaa gcatgaaaat  240
217 attgttgccc tggaagacat ttatgaaagc ccaaatcacc tgtacttggt catgcagctg  300
218 gtgtccggtg gagagctgtt tgaccggata gtggagaagg ggtttttatac agagaaggat  360
219 gccagcactc tgatccgcca agtcttggac gccgtgtact atctccacag aatgggcatc  420
220 gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa  480
221 ataatgatca gtgactttgg attgtcaaaa atggagggca aaggagatgt gatgtccact  540
222 gcctgtggaa ctccaggcta tgtcgctcct gaagtcctcg cccagaaacc ttacagcaaa  600
223 gccgttgact gctggtccat cggagtgatt gcctacatct tgctctgcgg ctaccctcct  660
224 ttttatgatg aaaatgactc caagctcttt gagcagatcc tcaaggcgga atatgagttt  720
225 gactctccct actgggatga catctccgac tctgcaaaag acttcattcg gaacctgatg  780
226 gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct  840
227 ggtgacacag ccctcaacaa aaacatccac gagtccgtca gcgcccagat ccggaaaaac  900
228 tttgccaaga gcaaatggag acaagcattt aatgccacgg ccgtcgtgag acatatgaga  960
229 aaactacacc tcggcagcag cctggacagt tcaaatgcaa gtgtttcgag cagcctcagt 1020
230 ttggccagcc aaaaagactg tgcgtatgta gcaaaaccag aatccctcag ctga        1074
232 <210> SEQ ID NO: 4
233 <211> LENGTH: 3579
234 <212> TYPE: DNA
235 <213> ORGANISM: Human
237 <220> FEATURE:
238 <221> NAME/KEY: 5'UTR
239 <222> LOCATION: (1)...(1212)
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01152002\J024036.raw

```
241 <221> NAME/KEY: CDS
242 <222> LOCATION: (1213)...(3159)
244 <221> NAME/KEY: 3'UTR
245 <222> LOCATION: (3160)...(3579)
247 <400> SEQUENCE: 4
248 aacagttctg tcacttggtc gacatttaat acatgtgagt tgtatgaatg cctaaaggcc 60
249 ataccatgct gcctgggaaa cagcaagaac tccatcagtg gcagagacta tcactattat 120
250 tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttggag ggaaaaagta 180
251 cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
252 gctgattttg gacttgcaaa gcatgtggtg agacctatat ttactgtgtg tgggacccca 300
253 acttacgtag ctcccgaaat tctttctgag aaaggttatg gactggaggt ggacatgtgg 360
254 gctgctggcg tgatcctcta tatcctgctg tgtggctttc ccccattccg cagccctgag 420
255 agggaccagg acgagctctt taacatcatc cagctgggcc actttgagtt cctccccct 480
256 tactgggaca atatctctga tgctgctaaa gatctggtga ccggttgct ggtggtagac 540
257 cccaaaaagc gctacacagc tcatcaggtt cttcagcacc cctggatcga aacagctggc 600
258 aagaccaata cagtgaaacg acagaagcag gtgtccccca gcagcgaggg tcacttccgg 660
259 agccagcaca agagggttgt ggagcaggta tcatatcygc tgagggctca agatgtgtct 720
260 cttaaagccc caaattccca ctcaacttct catagccatt atgactgatt tagctgaata 780
261 accttgggac agcaaggcct atgtgaccat tctctaaaat atttaagctc gagaatcaca 840
262 gagcggaagc tgcaaggctc ctggctgcct gccagccgag ggaatctgga gaaaccattc 900
263 ctggggccgc gtggccccgt cgtgcccttg ttctgccctc ggaatggcct tcactcagca 960
264 catcctgaga acagccctct gaagcccagg gtcgtgaccg tagtgaagct gggtgggcag 1020
265 cgcccccgaa agatcactct gctcctcaac aggcgatcag tgcagacgtt cgagcagctc 1080
266 ttagctgaca tctcagaagc cttgggctct cccagatgga agaatgaccg tgtgaggaaa 1140
267 ctgtttaacc tcaagggcag ggaaatcagg agcgtctctg atttcttcag ggaaggggat 1200
268 gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
269                 Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
270                  1           5                   10
272 gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc    1299
273 Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
274     15                  20                  25
276 cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc    1347
277 Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
278 30                  35                  40                  45
280 aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag    1395
281 Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
282                  50                  55                  60
284 agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg    1443
285 Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
286                  65                  70                  75
288 aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag    1491
289 Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
290                  80                  85                  90
292 aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc    1539
293 Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
294     95                  100                 105
296 agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt    1587
297 Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
298 110                 115                 120                 125
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/024,036

DATE: 01/15/2002
TIME: 18:18:41

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF3\01152002\J024036.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```